

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/017,085

DATE: 01/03/2002
 TIME: 13:09:57

Input Set : A:\Seq_Listing_for_P2630P1C73.wpd
 Output Set: N:\CRF3\01032002\J017085.raw

3 <110> APPLICANT: Ashkenazi, Avi
 4 Baker Kevin P.
 5 Botstein, David
 6 Desnoyers, Luc
 7 Eaton, Dan
 8 Ferrara, Napoleon
 9 Filvaroff, Ellen
 10 Fong, Sherman
 11 Gao, Wei-Qiang
 12 Gerber, Hanspeter
 13 Gerritsen, Mary E.
 14 Goddard, Audrey
 15 Godowski, Paul J.
 16 Grimaldi, J. Christopher
 17 Gurney, Austin L.
 18 Hillan, Kenneth J
 19 Kljavin, Ivar J.
 20 Kuo, Sophia S.
 21 Napier, Mary A.
 22 Pan, James;
 23 Paoni, Nicholas F.
 24 Roy, Margaret Ann
 25 Shelton, David L.
 26 Stewart, Timothy A.
 27 Tumas, Daniel
 28 Williams, P. Mickey
 29 Wood, William I.
 31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 32 Acids Encoding the Same
 34 <130> FILE REFERENCE: P2630P1C73
 36 <140> CURRENT APPLICATION NUMBER: US/10/017,085

 36 <141> CURRENT FILING DATE: 2001-10-24
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 57 <150> PRIOR APPLICATION NUMBER: 60/077641

Does Not Comply
Corrected Diskette Needed

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Output Set: N:\CRF3\01032002\J017085.raw

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,085

DATE: 01/03/2002
TIME: 13:09:57

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Output Set: N:\CRF3\01032002\J017085.raw

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Please correct subsequent
date errors

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/017,085

DATE: 01/03/2002
TIME: 13:09:57

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10/085

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<213> Artificial

<400> 157

see item 11 on Error Summary Sheet

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VERIFICATION SUMMARY
PATENT APPLICATION: US/10/017,085

DATE: 01/03/2002
TIME: 13:09:58

Input Set : A:\Seq_Listing_for_P2630P1C73.wpd
Output Set: N:\CRF3\01032002\J017085.raw

L:36 M:270 C: Current Application Number differs, Replaced Current Application No
L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:244 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:370 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:445 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:978 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
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L:6196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:151
L:6223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152
L:6225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:152

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/017,085

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L:6387 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:157
L:6389 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:6389 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:7719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:7729 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:8724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:10653 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10655 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10657 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>101017,085</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE.		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Sequence(s) missing. If Intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 <input type="checkbox"/> Invalid <213> Response	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input checked="" type="checkbox"/> Use of <220>	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Sequence(s) <u>157</u> missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
13 <input type="checkbox"/> Misuse of n!	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.